

00431PHRM293.ST25  
SEQUENCE LISTING

<110> Vogeli, Gabriel  
Huff, Rita  
Sejlitz, Torsten  
Lind, Peter  
Slightom, Jerry  
Schellin, Kathleen  
Bannigan, Chris  
Ruff, Valerie  
Kaytes, Paul  
Wood, Linda  
Parodi, Luis  
Hiebsch, Ronald

<120> Novel G Protein Coupled Receptors

<130> 00431PHRM293

<150> 60/165,838

<151> 1999-11-16

<150> 60/198,568

<151> 2000-04-20

<150> 60/166,071

<151> 1999-11-17

<150> 60/166,678

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&lt;151&gt; 2000-05-02

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&lt;151&gt; 2000-05-08

&lt;150&gt; 60/207,094

&lt;151&gt; 2000-05-25

&lt;160&gt; 190

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 1182

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 1

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ttctctgccc ttaccgtctt agccatcaaa ctctgagctg gagatagtga cgatgtgaca      180
ggaactttcc ctgggcctct ctgggccaca attcctggcc gagagaaaga ggaggaatga      240
ggtgagcacc ttcttctact ctagggccat gtggtagagc tgcagtcgca cctccttctg      300
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ccgttccagc actaggtaga ggtgacactc ctggcaggcc acctgcacaa tgccagtgat      420
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20          25          30
Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
35          40          45
Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
50          55          60
Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65          70          75          80
Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
85          90          95
Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
100         105         110
Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
115         120         125
Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
130         135         140
Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
145         150         155         160
Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
165         170         175
Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
180         185         190
Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
195         200         205
Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
210         215         220
Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
225         230         235         240
Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
245         250         255
Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
260         265         270
Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu

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275

280

285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
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Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu  
 305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
 325 330 335

&lt;210&gt; 3

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 3

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 gagcgtggcg gtgaaggctg cgaagcgcgg acgctcaggc tcggggcggca ggcgcagcga 180  
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 gctcagcgcc gcgttggacg ccaggaaggt gtccaggaag ccaatgactt ggcatgcgcc 420  
 gggcgccgac ggtgtccgcc cgcgcacac accgagcagc gtgaagggca tgtccagcgc 480  
 cgccagcagc aggtggccca gagacagatt caccaggagg acgcctgagg ctcgagtgcg 540  
 gagctcagcg ctgtaggcgc aacaaagcag caccagtgcg ttggatagca gcgccacggc 600  
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&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; H.Sapiens

&lt;400&gt; 4

Ser Ala Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met  
 1 5 10 15

Val Leu Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys  
 20 25 30

Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val  
 35 40 45

Asn Leu Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe  
 50 55 60

## 00431PHRM293.ST25

Thr Leu Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala  
65 70 75 80

Cys Gln Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala  
85 90 95

Leu Ser Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe  
100 105 110

Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu  
115 120 125

Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu  
130 135 140

Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu  
145 150 155 160

Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala  
165 170 175

Thr Leu His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu  
180 185 190

Thr Ser Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met  
195 200 205

Asp Thr Val Thr Met Lys Ala Leu Ala  
210 215

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tataacattg tcctcatcag ctatgatcga tacctgtcag tctcaaagtc tgtaagtcga 180  
acacattaat ttatccccct tagaagatta tgtaaagtga ta 222

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<212> PRT  
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Glu Trp Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp  
20 25 30

Tyr Leu Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr

35

40

45

Asp Arg Tyr Leu Ser Val Ser Asn Ala Val Ser Arg Thr His Phe Ile  
 50 55 60

Pro Leu Arg Arg Leu Cys Lys Cys Ile  
 65 70

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 acgacggcgg cgccagcgct tggagctgag cgggtacagg atccccagga agcgctccac 180  
 gctgatacag gtcattggtga ggatgctgga atacatgttt gcgtaaaagg ccacgggtcac 240  
 cacgttgcaa agcagcacccc cgaataccca gtggtggcgg ttgcaatggt agtagatttg 300  
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 cgacggggat ctggggcccca tgcgccggca cagcaccac agagagaaga gggtgcccgg 420  
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 ccgcagcatc tgcagcgctc cgttgctc 507

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<400> 8

Asp Asn Ala Thr Leu Gln Met Leu Arg Asn Pro Ala Ile Ala Val Ala  
 1 5 10 15

Leu Pro Val Val Tyr Ser Leu Val Ala Ala Val Ser Ile Pro Gly Asn  
 20 25 30

Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro  
 35 40 45

Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala  
 50 55 60

Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp  
 65 70 75 80

Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala  
 85 90 95

Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg

100

105

110

Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg  
 115 120 125

Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr  
 130 135 140

Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala  
 145 150 155 160

Leu Gly Ile Ile Thr Cys Phe Asp Val  
 165

<210> 9  
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 gcacgggagg gaggcgtctt cgtggcactc actgcgtccg tgctgagcct cctgggcac 180  
 gcgctggagc gcagcctcac catggcgcgcg aggggggccc cgcccgctctc cagtcggggg 240  
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<210> 10  
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 20 25 30  
 Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val  
 35 40 45  
 Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Glu Arg  
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 65 70 75 80  
 Arg Thr Leu Ala Met Ala Ala Ala Ala Trp  
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&lt;400&gt; 11

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gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac      180
tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc      240
gggagcatcg tgttccttac ggtgggtggct gcggacaggt atttcaaagt ggtccacccc      300
caccacgcgg tgaacactat ctccacccgg gtggcggtctg gcatcgtctg caccctgtgg      360
gccctgggtca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag      420
acggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg      480
ttccagctgg agttctttat gcccctcggc atcatcttat tttgctcctt caagattggt      540
tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgacccgg      600
ttcatcatgg tggtaggcaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga      660
ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg      720
cacataaccc tcagcttcac ctacatgaac agcatgctgg atccccctgg gtattatttt      780
tcaagcccct cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag      840
cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcg      888

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&lt;210&gt; 12

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; H.Sapiens

&lt;400&gt; 12

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1          5          10          15
Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys Pro Ser Thr Val
20          25          30
Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu
35          40          45
Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly
50          55          60
Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala
65          70          75          80
Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys
85          90          95

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Val Val His Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala  
100 105 110

Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val  
115 120 125

Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser  
130 135 140

Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met  
145 150 155 160

Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser  
165 170 175

Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln  
180 185 190

Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val  
195 200 205

Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu  
210 215 220

Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu  
225 230 235 240

His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu  
245 250 255

Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu  
260 265 270

Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln  
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Arg Pro Glu Glu Met Pro Ile Ser  
290 295

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<212> DNA

<213> H.Sapiens

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tgcaagctgg tgcacttcct gttctatata aacctttacg gcagcatcct gctgctgacc 180

tgcattctctg tgcaccagtt cctaggtgtg tgccaccacac tgtgttcgct gccctaccgg 240

acccgcaggc atgcctggct gggcaccagc accacctggg ccctggtggt cctccagctg 300

ctgcccacac tggccttctc ccacacggac tacatcaatg gccagatgat ctggtatgac 360

atgaccagcc aagagaattt tgatcggtt tttgcctacg gcatagttct gacattgtct 420

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Arg Trp Pro Phe Gly Glu Leu Leu Cys Lys Leu Val His Phe Leu Phe  
35 40 45  
Tyr Ile Asn Leu Tyr Gly Ser Ile Leu Leu Leu Thr Cys Ile Ser Val  
50 55 60  
His Gln Phe Leu Gly Val Cys His Pro Leu Cys Ser Leu Pro Tyr Arg  
65 70 75 80  
Thr Arg Arg His Ala Trp Leu Gly Thr Ser Thr Thr Trp Ala Leu Val  
85 90 95  
Val Leu Gln Leu Leu Pro Thr Leu Ala Phe Ser His Thr Asp Tyr Ile  
100 105 110  
Asn Gly Gln Met Ile Trp Tyr Asp Met Thr Ser Gln Glu Asn Phe Asp  
115 120 125  
Arg Leu Phe Ala Tyr Gly Ile Val Leu Thr Leu Ser Gly Phe Leu Ser  
130 135 140  
Leu Leu Gly His Phe Gly Val Leu Phe Thr Asp Gly Gln Glu Pro Asp  
145 150 155 160  
Gln Ala Arg Gly Glu Pro His Glu Asp Arg  
165 170

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<223> n is any nucleotide

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ggctccacct gggctcgccg accaggccgc tgcacccgct ggggccttca gccggtgccg 240
ccaccagacg gagagtaggt ggccacaagc gacacccatg atcttaacag gcgcgacgaa 300
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gatccagtgg cagcgacgca tccccggcca ggctcgggcg gagagtggcg cgctggctg 420
cagagacggt nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nagtactagc gcaccacaaa 480
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cgtgcccccg cacgcgtaca ggtccgccag ggccagctgc accagcagga agtccatctt 780
gcgacgcttn nnnnnnnnnn nnnnnnnnnn nnnnnnnnac aggcggcaca gcaactgtgt 840
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<400> 16

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Arg Val Arg Leu Val Phe Leu Gly Val Ile Leu Val Val Ala Val Ala
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Gly Asn Thr Thr Val Leu Cys Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20          25          30

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Xaa Xaa Xaa Lys Arg Arg Lys Met Asp Phe Leu Leu Val Gln Leu Ala
35          40          45

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Leu Ala Asp Leu Tyr Ala Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala
50          55          60

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Trp Glu Leu Leu Gly Glu Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys  
 65 70 75 80  
 Arg Phe Leu Gln Leu Leu Gln Ala Ser Gly Arg Gly Ala Ser Ala His  
 85 90 95  
 Leu Val Val Leu Ile Ala Leu Glu Arg Arg Arg Ala Val Arg Leu Pro  
 100 105 110  
 His Gly Arg Pro Leu Pro Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu  
 115 120 125  
 Leu Ala Leu Leu Leu Ala Arg Gly Ser Gly Phe Val Val Arg Tyr Xaa  
 130 135 140  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Leu Gln Pro Gly  
 145 150 155 160  
 Ala Pro Leu Ser Ala Arg Ala Trp Pro Gly Met Arg Arg Cys His Trp  
 165 170 175  
 Ile Phe Ala Leu Leu Gln Arg Trp His Val Gln Val Tyr Ala Phe Tyr  
 180 185 190  
 Glu Ala Val Ala Gly Phe Val Ala Pro Val Lys Ile Met Gly Val Ala  
 195 200 205  
 Cys Gly His Leu Leu Ser Val Trp Trp Arg His Arg Leu Lys Ala Pro  
 210 215 220  
 Ala Gly Ala Ala Ala Trp Ser Ala Ser Pro Gly Gly Ala Arg Ala Pro  
 225 230 235 240  
 Ser Ala Met Pro Arg Ala Lys Val Gln Ser Leu Lys Met Ser Gln Leu  
 245 250 255  
 Leu Gly Leu Leu Phe Val Gly Cys Glu Leu Pro Phe Ala Asp Arg Leu  
 260 265 270  
 Glu Ala Ala Trp Ser Ser Gly Pro Ala Gly Glu Trp Glu Gly Glu Ala  
 275 280 285  
 Leu Ser Ala Cys Cys Ala Trp Trp  
 290 295

&lt;210&gt; 17

&lt;211&gt; 801

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 17

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ggggaggagg tagaatagga aggagggtgac ctggatgatg aaattgtaga tccacatggg 180

cttgatgacc gtacaggtgg ccgaacctgg gaccagggac ccattgggga agtagtgga 240

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cttgatgccca tggatgctgg tgttgggcag ggagaagagc acggagaagc cccagacgat      300
gccgaggatc ctgagggccc ggcgccgggt gctctgcagt ttggcgcgga acgggtgtag      360
gatggccacg tagcgctcca cgctgacggt ggtgatgctg aggatggagg cgaagcacac      420
ggtctcaaag agggccgtct tgaagtagca gcccacgggc ccgaacaaga aagggtagtt      480
gcgccacatc tcatagacct ccaggggcat tccaaggagc aggaccagga ggtagagac      540
cgccaggctg aagaggtagt agttgggtgg cgtcttcata gcctgggtgct gcagaatcac      600
caggcacacc aggacattgc caatgacccc caccacaaaa attggcacat acaccacaga      660
cacggggagg aagaagtggc tgcgccgagg tccgcagagg aaggccagat actcctcggt      720
gctgttcagg tgtttctgga atggatcttc tagtttctgc tggtagatcc aggaagcatt      780
ctgaagtttt tccatccctg a                                              801

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<210> 18
<211> 249
<212> PRT
<213> H.Sapiens

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<400> 18

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Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
1          5          10          15
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
20          25          30
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
35          40          45
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
50          55          60
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Asn Thr
65          70          75          80
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
85          90          95
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu
100          105          110
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val
115          120          125
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
130          135          140
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
145          150          155          160

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## 00431PHRM293.ST25

Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe  
165 170 175

Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro  
180 185 190

Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro  
195 200 205

Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr  
210 215 220

Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu  
225 230 235 240

Arg Val Ser Ile Ala Gly Val Ala Gly  
245

<210> 19  
<211> 222  
<212> DNA  
<213> H.Sapiens

<400> 19  
atcaagatga tttttgctat cgtgcaaatt attggatttt ccaactccat ctgtaatccc 60  
attgtctatg catttatgaa tgaaaacttc aaaaaaatg ttttgtctgc agtttggtat 120  
tgcatagtaa ataaaacctt ctctccagca caaaggcatg gaaattcagg aattacaatg 180  
atgcggaaga aagcaaagtt ttccctcaga gagaatccag tg 222

<210> 20  
<211> 73  
<212> PRT  
<213> H.Sapiens

<400> 20

Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser  
1 5 10 15

Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys  
20 25 30

Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser  
35 40 45

Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys  
50 55 60

Ala Lys Phe Ser Leu Arg Glu Asn Pro  
65 70

<210> 21  
<211> 447  
<212> DNA  
<213> H.Sapiens

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<210> 27
<211> 420
<212> DNA
<213> H.Sapiens

<220>
<221> misc_feature
<222> (81)..(106)
<223> n is any nucleic acid
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tcgcgggtcc	gcagcctcct	nnnnnnnnnn	nnnnnnnnnn	nnnnntggc	agagcttgcg	120	
cgcgatgcgg	gcgtacatga	ccacgatgag	cgccagcggc	gccaggtaga	tgtgcgagaa	180	
gagcacagtg	gtgtagaccc	tcgcatgcc	cttctcgggc	caggcctccc	agcaggagta	240	
gagagggtag	gagcggttgc	gggcgtccac	catgaagtgg	tgctcctcac	gggtgacggt	300	
cagcgtgacg	gccgagggac	acatgatgag	cagcgccagg	gccagatga	cggcgatggt	360	
gacgagcgcc	ttccgcaggg	tcagcttctc	gcggaagg	tgacgatgc	agcggaacct	420	

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<210> 28
<211> 139
<212> PRT
<213> H.Sapiens

<220>
<221> UNSURE
<222> (104)..(113)
<223> Xaa is Unknown
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<400> 28
Phe Arg Cys Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys
1           5           10          15
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Ala Leu Val Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met  
20 25 30

Cys Pro Ser Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe  
35 40 45

Met Val Asp Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu  
50 55 60

Ala Trp Pro Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe  
65 70 75 80

Ser His Ile Tyr Leu Ala Pro Leu Ala Leu Ile Val Val Met Tyr Ala  
85 90 95

Arg Ile Ala Arg Lys Leu Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
100 105 110

Xaa Glu Ala Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val  
115 120 125

His Met Leu Val Met Val Ala Leu Phe Phe Thr  
130 135

<210> 29  
<211> 318  
<212> DNA  
<213> H.Sapiens

<400> 29  
gcagggggcg tgagtcctca ggcacttctt gaggtccttg ttgagcagga agcagacaat 60  
tgggttgacg gcagcctggg cgaagctcat ccaaacagca gtggccaggt agcgggtggg 120  
cacagcacag gctttcacaa aactcgcga gtagcaggcc acgatgtagg gtgaccagag 180  
gagcagaaaag agcagtgtga tcgcgtagaa catgçggccc agctgctttt cacccttgac 240  
ctcgccatg cccagtagcc gccggctggc tgcatgccc ttctgccgga taccagcag 300  
ggttggtggc atgggccc 318

<210> 30  
<211> 106  
<212> PRT  
<213> H.Sapiens

<400> 30

Gly Pro Met Pro Pro Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala  
1 5 10 15

Ala Ser Arg Arg Leu Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln  
20 25 30

Leu Gly Arg Met Phe Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp  
35 40 45



## 00431PHRM293.ST25

Ser Pro Tyr Ile Val Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys  
50 55 60

Ala Val Pro His Arg Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala  
65 70 75 80

Gln Ala Ala Val Asn Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu  
85 90 95

Lys Lys Cys Leu Arg Thr His Ala Pro Cys  
100 105

<210> 31  
<211> 354  
<212> DNA  
<213> H.Sapiens

<400> 31  
tattctgtaa tgaagaatgt cattcacact gccattggca catccagtgg cctcacctag 60  
cattgtgaaa gcccttcggt tgggtgtattg ccacttcatt ttaaaaggat gcacaagtcc 120  
ctggtgcctt tccacagcaa tgcaggtcat agtgaggatt tctgtcacia cagcggtaga 180  
ctggacaaat ggcaccatct tgcaaatgaa agcacctgca gtaaggaaat aggataaatc 240  
atacatcaaa acaaaaagaa taaaggtttc atctgtgtct ttgtaattat cactatcagt 300  
ccattctgag cctctgccaa aaagtttgat aattgtaatt actctgtaga caca 354

<210> 32  
<211> 117  
<212> PRT  
<213> H.Sapiens

<400> 32

Val Tyr Arg Val Ile Thr Ile Ile Lys Leu Phe Gly Arg Gly Ser Glu  
1 5 10 15

Trp Thr Asp Ser Asp Asn Tyr Lys Asp Thr Asp Glu Thr Phe Ile Leu  
20 25 30

Phe Val Leu Met Tyr Asp Leu Ser Tyr Phe Leu Thr Ala Gly Ala Phe  
35 40 45

Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu  
50 55 60

Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val  
65 70 75 80

His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr  
85 90 95

Met Leu Gly Glu Ala Thr Gly Cys Ala Asn Gly Ser Val Asn Asp Ile  
100 105 110

Leu His Tyr Arg Ile  
115

<210> 33  
<211> 621  
<212> DNA  
<213> H.Sapiens

<400> 33  
gagcaacatg atctttttga agtacttgac ggtgtcgttc ttgacgggtca cgaagcacag 60  
agtgttgatc atgctgttgc tcatggcgat gcactcgacg atgtagaagg cagtgaggta 120  
gtgcttctcc ttcacaaaca cgggtgggaa gaagtcgagc acgatgggtga agccgtagaa 180  
gggcgcccag catagcacgt aggcgggtgag gatgcacatg agcaccagga ccgtcttcct 240  
gcggcagcgc agcctcttgc ggatctgctc tgtctggaat ccagggaccg ccttgaacca 300  
gagctcccg g gatcctgg catagcacag ggtcatgggtg accacggggc ccacgaattc 360  
tatgccaaag ataaagagga agtaggactt gtagtagagc tgctggtcca caggccagat 420  
ctggccgcag aagatctttt cctgggtctt gacaatgacg aggaccgtct cggtggtgaa 480  
gtaggcggaa gggatggcga tcaggatgga caccgtccac accaaggcaa tcaggccagt 540  
ggctgtttgg cacttcattc gtggtctcag cggatggaca atagccagat acctagggca 600  
agaacacaag tggaggcagc c 621

<210> 34  
<211> 207  
<212> PRT  
<213> H.Sapiens

<400> 34  
Gly Cys Leu His Leu Cys Ser Cys Pro Arg Tyr Leu Ala Ile Val His  
1 5 10 15  
Pro Leu Arg Pro Arg Met Lys Cys Gln Thr Ala Thr Gly Leu Ile Ala  
20 25 30  
Leu Val Trp Thr Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe  
35 40 45  
Thr Thr Glu Thr Val Leu Val Ile Val Lys Ser Gln Glu Lys Ile Phe  
50 55 60  
Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr  
65 70 75 80  
Phe Leu Phe Ile Phe Gly Ile Glu Phe Val Gly Pro Val Val Thr Met  
85 90 95  
Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val

100

105

110

Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg  
 115 120 125

Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys  
 130 135 140

Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr  
 145 150 155 160

Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu  
 165 170 175

Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr  
 180 185 190

Val Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu  
 195 200 205

<210> 35  
 <211> 483  
 <212> DNA  
 <213> H.Sapiens

<400> 35  
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 taagaagcca caaaaacttcc cttccagggt gttcagcagc agggacaggg cccagggcag 120  
 ggcacacatg acagttgaca ggtttcttgg gcagcagcag cagtaccaga taggccgcag 180  
 gacagacagg cagcactcag tactgatggc actcagcatg ctcaggccta caaggtaggc 240  
 aaaggtcac acgctggtga agaagctagg gaaattgatg gagatggaac agaagaagtt 300  
 actgaggtac accaggcaat ttataatctg gaagcagagg aagaggaagt cggccccggc 360  
 caggctgagg acgtagacag agaaggcgtt cctgcgcagc cggaagccca ggagccagag 420  
 cacaaacccg tttcctacga gcccagaccag ggcaatgaaa aggatcagga agaccgggat 480  
 cag 483

<210> 36  
 <211> 161  
 <212> PRT  
 <213> H.Sapiens

<400> 36

Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val  
 1 5 10 15

Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn  
 20 25 30

Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe

35

40

45

Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe  
 50 55 60  
 Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Ser Val Met Thr  
 65 70 75 80  
 Phe Ala Tyr Leu Val Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu  
 85 90 95  
 Cys Cys Leu Ser Val Leu Arg Pro Ile Trp Tyr Cys Cys Cys Cys Pro  
 100 105 110  
 Arg Asn Leu Ser Thr Val Met Cys Ala Leu Pro Trp Ala Leu Ser Leu  
 115 120 125  
 Leu Leu Asn Thr Leu Glu Gly Lys Phe Cys Gly Phe Leu Val Ser Asn  
 130 135 140  
 Gly Asp Tyr Gly Trp Cys Trp Thr Phe Asp Phe Ile Thr Ala Val Trp  
 145 150 155 160

Leu

<210> 37  
 <211> 330  
 <212> DNA  
 <213> H.Sapiens

<400> 37  
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 atcctttgct tgtccgttga ggtcctagtc tggagccaag tgacaaagac agagatcacc 120  
 tatttacgcc atgtgtgcat tgtaacatt gcagccactt tgctgatggc agatgtgtgg 180  
 ttcatgtgg cttcctttct tagtggccca ataacacacc acaagggatg tgtggcagcc 240  
 acattttttg gtcatttctt ttacctttct gtatttttct ggatgcttgc caaggcactc 300  
 cttatcctct atggaatcat gattgttttc 330

<210> 38  
 <211> 110  
 <212> PRT  
 <213> H.Sapiens

&lt;400&gt; 38

Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr Val Gly Leu Gly Ile Ser  
 1 5 10 15  
 Ile Cys Ser Leu Ile Leu Cys Leu Ser Val Glu Val Leu Val Trp Ser  
 20 25 30  
 Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu Arg His Val Cys Ile Val

35

40

45

Asn Ile Ala Ala Thr Leu Leu Met Ala Asp Val Trp Phe Ile Val Ala  
50 55 60

Ser Phe Leu Ser Gly Pro Ile Thr His His Lys Gly Cys Val Ala Ala  
65 70 75 80

Thr Phe Phe Gly His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met Leu  
85 90 95

Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile Met Ile Val Phe  
100 105 110

&lt;210&gt; 39

&lt;211&gt; 628

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 39

ttgtgtggca gtagagagat gtcaggcttc agagtcaaca agaactggat ttcaaactgg 60  
at ttgaggac cccacaccttt ggtaagtgc ttattatctg cgagcctctg tttctctctt 120  
ctttaaatga ggacagtaaa tcccatacgg caggggtggtg gggagaatca gagatgatac 180  
agctggtgat cacatctggt ttgtgttccc aggggcacca gactagggtt tctgagcatg 240  
gatccaaccg tcccagtctt cggtacaaaa ctgacaccaa tcaacggacg tgaggagact 300  
ccttgctaca atcagaccct gagcttcacg gtgctgacgt gcatcatttc ccttgctcgga 360  
ctgacaggaa acgcggtagt gctctggctc ctgggctacc gcatgcgcag gaacgctgtc 420  
tccatctaca tcctcaacct ggccgcagca gacttcctct tcctcagctt ccagattata 480  
cgttcgccat tacgcctcat caatatcagc catctcatcc gcaaaatcct cgtttctgtg 540  
atgaccttc cctactttac aggcctgagt atgctgagcg ccatcagcac cgagcgctgc 600  
ctgtctgttc tgtggcccat ctggtacc 628

&lt;210&gt; 40

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; H.Sapiens

&lt;400&gt; 40

Leu Cys Gly Ser Arg Glu Met Ser Gly Phe Arg Val Asn Lys Asn Trp  
1 5 10 15

Ile Ser Asn Trp Ile Gly Pro Pro Pro Leu Val Ser Asp Leu Leu Ser  
20 25 30

Ala Ser Leu Cys Phe Ser Leu Leu Met Arg Thr Val Asn Pro Ile Arg  
35 40 45

## 00431PHRM293.ST25

Gln Gly Gly Gly Glu Asn Gln Arg Tyr Ser Trp Ser His Leu Val Cys  
50 55 60

Val Pro Arg Gly Thr Arg Leu Gly Phe Leu Ser Met Asp Pro Thr Val  
65 70 75 80

Pro Val Phe Gly Thr Lys Leu Thr Pro Ile Asn Gly Arg Glu Glu Thr  
85 90 95

Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile  
100 105 110

Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly  
115 120 125

Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala  
130 135 140

Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Ser Pro Leu  
145 150 155 160

Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val  
165 170 175

Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser  
180 185 190

Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr  
195 200 205

<210> 41  
<211> 319  
<212> DNA  
<213> H.Sapiens

<400> 41  
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ctgcccttct ttgtcttgac gatcacagat cctttcatta attttacaac ctttgaagat 120  
ctgtacaatg tcttcctcctg gctaggctat ttcaactctg ctttcaatcc cattttatat 180  
ggcatgcttt atccttggtt tcgcaaggca ttgaggatga ttgtcacagg catgatcttc 240  
caccctgact cttccaccct aagcctgttt tctgcccattg cttaggctgt gttcatcatt 300  
caataggact cttttctgg 319

<210> 42  
<211> 103  
<212> PRT  
<213> H.Sapiens

<400> 42

Thr Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe  
1 5 10 15

## 00431PHRM293.ST25

Val Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe  
 20 25 30  
 Ile Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu  
 35 40 45  
 Gly Tyr Phe Asn Ser Ala Phe Asn Pro Ile Leu Tyr Gly Met Leu Tyr  
 50 55 60  
 Pro Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe  
 65 70 75 80  
 His Pro Asp Ser Ser Thr Leu Ser Leu Phe Ser Ala His Ala Ala Val  
 85 90 95  
 Phe Ile Ile Gln Asp Ser Phe  
 100

<210> 43  
 <211> 515  
 <212> DNA  
 <213> H.Sapiens

<400> 43  
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 gaatcagcaa atcttattca cttatcacta aatctaaaat atgtcaaaat acatgaagac 120  
 aacaaatgct ttagaacaac tggtgaatgt attgtcctac aacttggcat atgatcatgc 180  
 ttgcctctct atgtccaagt gtttattttt gcagttgacc ttaatttcaa gttagttttg 240  
 aggtctctac agtaatgttt ttaatctgtc tctacttctt cagaaaataa attagttgtt 300  
 gacgaatcag tccttaagac cttgccgctt acaataagtt ttattgcctt cccaaacccat 360  
 tggtaaaaga aagcataaat caaggggttc atagctgaat tataataaac acaccaaact 420  
 aaaatctcat aaacataagg aggagttata aaattcatat aagcatcaat cactgcatca 480  
 acgaggtatg gtagccaaga gacaagaaat gctgc 515

<210> 44  
 <211> 148  
 <212> PRT  
 <213> H.Sapiens

<400> 44

Leu His Gln Arg Gly Met Val Ala Lys Arg Gln Glu Met Leu Ala Ala  
 1 5 10 15  
 Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala  
 20 25 30  
 Tyr Met Asn Phe Ile Thr Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp  
 35 40 45

## 00431PHRM293.ST25

Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe  
50 55 60

Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val  
65 70 75 80

Leu Arg Thr Asp Ser Ser Thr Thr Asn Leu Phe Ser Glu Glu Val Glu  
85 90 95

Thr Asp Lys His Tyr Cys Arg Asp Leu Lys Thr Asn Leu Lys Leu Arg  
100 105 110

Ser Thr Ala Lys Ile Asn Thr Trp Thr Arg Gly Lys His Asp His Met  
115 120 125

Pro Ser Cys Arg Thr Ile His Ser Thr Val Val Leu Lys His Leu Leu  
130 135 140

Ser Ser Cys Ile  
145

<210> 45  
<211> 726  
<212> DNA  
<213> H.Sapiens

<400> 45  
ctggaaagag gtcctcgatc taccctctac gccgtccttg gttttggggc tgtgctggca 60  
gcgtttggaa acttactggt catgattgct atccttcact tctaacaact gcacacacct 120  
acaaactttc tgattgcgtc gctggcctgt gctgacttct tgggtgggagt cactgtgatg 180  
cccttcagca cagtgaggtc tgtggagagc tgttggtact ttggggacag ttactgtaaa 240  
ttccatacat gttttgacac atctttctgt tttgcttctt tatttcattt atgctgtatc 300  
tctgttgata gatacattgc tgttactgat cctctgacct atccaaccaa gtttactgtg 360  
tcagtttcag ggatatgcat tgttctttcc tggttctttt ctgtcacata cagcttttcg 420  
atcttttaca cgggagccaa cgaagaagga attgaggaat tagtagttgc tctaacctgt 480  
gtaggaggct gccaggctcc actgaatcaa aactgggtcc tactttgttt tcttctattc 540  
tttataacca atgtcgccat ggtgtttata tacagtaaga ttttttggt ggccaagcat 600  
caggctagga agatagaaaag tacagccagc caagctcagt ccttctcaga gagttacaag 660  
gaaagagtag caaaaagaga gagaaaggct gccaaaacct tgggaattgc tatggcagca 720  
tttctt 726

<210> 46  
<211> 241  
<212> PRT  
<213> H.Sapiens



&lt;400&gt; 46

Leu Glu Arg Gly Pro Arg Ser Ile Leu Tyr Ala Val Leu Gly Phe Gly  
 1 5 10 15  
 Ala Val Leu Ala Ala Phe Gly Asn Leu Leu Val Met Ile Ala Ile Leu  
 20 25 30  
 His Phe Gln Leu His Thr Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala  
 35 40 45  
 Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Thr Val  
 50 55 60  
 Arg Ser Val Glu Ser Cys Trp Tyr Phe Gly Asp Ser Tyr Cys Lys Phe  
 65 70 75 80  
 His Thr Cys Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His Leu  
 85 90 95  
 Cys Cys Ile Ser Val Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Thr  
 100 105 110  
 Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Val Leu  
 115 120 125  
 Ser Trp Phe Phe Ser Val Thr Tyr Ser Phe Ser Ile Phe Tyr Thr Gly  
 130 135 140  
 Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys Val  
 145 150 155 160  
 Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys Phe  
 165 170 175  
 Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser Lys  
 180 185 190  
 Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr Ala  
 195 200 205  
 Ser Gln Ala Gln Ser Phe Ser Glu Ser Tyr Lys Glu Arg Val Ala Lys  
 210 215 220  
 Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala Phe  
 225 230 235 240  
 Leu

&lt;210&gt; 47

&lt;211&gt; 660

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 47

aaccaggtgg ccttactcct aagaccctg gccttgctta tggcctttat caacagctgt 60

ctcaatccag ttctctatgt cttcattggg catgacttct gggagcactt gctccactcc 120

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ctgctagctg ccttagaacg ggcacttagc gaggagccag atagtgcctg aatcccagct 180
cccaggcaga tgagtccttt ataacatgac ccaatttcct actccatttt cccaccactc 240
aatcctcttc ccaaacagct ctaccataat ccaacatcca acagaattta agagaataaa 300
ccacaacttt taagttagct ctatgtgcta ggtcatgttt tagaatacaa ccttaagtgc 360
ctggaagatg gaggcaagaa acaaacaagg tctcattctt tagaggaaga cagttcacca 420
agactcaaac agaaaaaaag atagttatct tgtgacaaaa caagtcataa aattgggtca 480
ggacctgcag caatgacttt atgctagaat ccagagcact agcaggaaaac tgcttaaatt 540
ttacttaatc aaagtcaagt ttggacatac atgtcaggta aaacctagca gagatgagct 600
accttgattt taaaacttca agggatagct caatgtcatc aagatccttt tgatgacttg 660

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<210> 48
<211> 211
<212> PRT
<213> H.Sapiens

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<400> 48

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Asn Gln Val Ala Leu Leu Leu Arg Pro Leu Ala Leu Ser Met Ala Phe
1          5          10          15
Ile Asn Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Ile Gly His Asp
20          25          30
Phe Trp Glu His Leu Leu His Ser Leu Leu Ala Ala Leu Glu Arg Ala
35          40          45
Leu Ser Glu Glu Pro Asp Ser Ala Ile Pro Ala Pro Arg Gln Met Ser
50          55          60
Pro Leu His Asp Pro Ile Ser Tyr Ser Ile Phe Pro Pro Leu Asn Pro
65          70          75          80
Leu Pro Lys Gln Leu Tyr His Asn Pro Thr Ser Asn Arg Ile Glu Asn
85          90          95
Lys Pro Gln Leu Leu Ser Glu Leu Tyr Val Leu Gly His Val Leu Glu
100         105         110
Tyr Asn Leu Lys Cys Leu Glu Asp Gly Gly Lys Lys Gln Thr Arg Ser
115         120         125
His Ser Leu Glu Glu Asp Ser Ser Pro Arg Leu Lys Gln Lys Lys Arg
130         135         140
Leu Ser Cys Asp Lys Thr Ser His Lys Ile Gly Ser Gly Pro Ala Ala
145         150         155         160
Met Thr Leu Cys Asn Pro Glu His Gln Glu Thr Ala Ile Leu Leu Asn
165         170         175

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Gln Ser Gln Val Trp Thr Tyr Met Ser Gly Lys Thr Gln Arg Ala Thr  
180 185 190

Leu Ile Leu Lys Leu Gln Gly Ile Ala Gln Cys His Gln Asp Pro Phe  
195 200 205

Asp Asp Leu  
210

<210> 49  
<211> 465  
<212> DNA  
<213> H.Sapiens

<400> 49  
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agcggaggcg cgcggtgggc ctggccgcgg tggctttgct ggcctttgtc acctgcttcg 120  
cccccaacaa cttcgtgctc ctggcgcaca tcgtgagccg cctgttctac ggcaagagct 180  
actaccacgt gtacaagctc acgctgtgtc tcagctgcct caacaactgt ctggaccctg 240  
ttgtttatta ctttgcgtcc cggaattcc agctgcgcct gcgggaatat ttgggctgcc 300  
gccgggtgcc cagagacacc ctggacacgc gccgcgagag cctcttctcc gccaggacca 360  
cgcccggtgcg ctccgaggcc ggtgcgcacc ctgaagggat ggaggagacc accaggcccc 420  
gcctccagag gcaggagagt gtgttctgag tcccgggggc gcagc 465

<210> 50  
<211> 160  
<212> PRT  
<213> H.Sapiens

<400> 50

Leu Phe Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu Glu Ala His  
1 5 10 15

Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala Val Val Leu  
20 25 30

Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val Leu Leu Ala  
35 40 45

His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr His Val Tyr  
50 55 60

Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu Asp Pro Phe  
65 70 75 80

Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu Arg Glu Tyr  
85 90 95

Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr Arg Arg Glu

100

105

110

Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu Ala Gly Ala  
 115 120 125

His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu Gln Arg Gln  
 130 135 140

Glu Ser Val Phe Val Pro Gly Ala Gln Ala Ala Pro Pro Gly Leu Arg  
 145 150 155 160

<210> 51  
 <211> 603  
 <212> DNA  
 <213> H.Sapiens

<400> 51  
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 ccggaaccca cagggcccccg tgggccatga gaggctcctg gacttgaacc tcaggacact 180  
 cccactctgg ctgccggcag ggatggaagc tggatgagca ggcaggagct ggcagtgggg 240  
 gtggagagcc ataggctatt ggggtggaca ggcttgggtg cctcatggga gctcccatg 300  
 ggagctgtgg ccccttgggg cctcttattt ctcaccccag gctttcccgg gagaggttca 360  
 agtcagaaga tgccccaaag atccacgtgg ccctgggtgg cagcctgttc ctctgaatc 420  
 tggccttctt ggtcaatgtg gggagtggct caaaggggtc tgatgctgcc tgctgggccc 480  
 ggggggctgt cttccactac ttctgtctct gtgccttcac ctggatgggc cttgaagcct 540  
 tccacctcta cctgctcgct gtcagggtct tcaacaccta cttcgggcac tacttctcta 600  
 agc 603

<210> 52  
 <211> 198  
 <212> PRT  
 <213> H.Sapiens

<400> 52

Glu Thr Tyr Ser Ala Leu Tyr Pro Thr Phe Asn Ser Leu Cys Tyr Ser  
 1 5 10 15

Pro Ala Ser Phe Ser Gly Leu Ile Phe Pro Ile Ile Leu Pro His Ile  
 20 25 30

Asp Gln Gly Met Arg Leu Ala Gly Ser Gly Thr His Arg Ala Pro Trp  
 35 40 45

Ala Met Arg Gly Ser Trp Thr Thr Ser Gly His Ser His Ser Gly Cys  
 50 55 60

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Arg Gln Gly Trp Lys Leu Asp Glu Gln Ala Gly Ala Gly Ser Gly Gly  
65 70 75 80

Gly Glu Pro Ala Ile Gly Val Asp Arg Leu Gly Cys Leu Met Gly Ala  
85 90 95

Pro His Gly Ser Cys Gly Pro Leu Gly Pro Leu Ile Ser His Pro Arg  
100 105 110

Leu Ser Arg Glu Arg Phe Lys Ser Glu Asp Ala Pro Lys Ile His Val  
115 120 125

Ala Leu Gly Gly Ser Leu Phe Leu Leu Asn Leu Ala Phe Leu Val Asn  
130 135 140

Val Gly Ser Gly Ser Lys Gly Ser Asp Ala Ala Cys Trp Ala Arg Gly  
145 150 155 160

Ala Val Phe His Tyr Phe Leu Leu Cys Ala Phe Thr Trp Met Gly Leu  
165 170 175

Glu Ala Phe His Leu Tyr Leu Leu Ala Val Arg Val Phe Asn Thr Tyr  
180 185 190

Phe Gly His Tyr Phe Leu  
195

<210> 53  
<211> 335  
<212> DNA  
<213> H.Sapiens

<400> 53  
aattggtcgg agagtgcagc tgcttgaaat ggaggattga aatcatcacc aggaggtttc 60  
caaacacagc cagcacagcc ccaaagccaa acactatgta cagaatcacc cgggatcccg 120  
gcgagaaggg gattttcaca caggacccat tcacgttcgc gtagcacagc tgcacagcca 180  
ccagcaggga tgaattgctg ctcataacgc tggatatttac atatggagaa attttgcct 240  
tggtgattat cacaaaaaat acaggattgt tcttgatttt cattgctcct gcggaaaaaa 300  
acacatattc accaggatgc cagaggaaat gatca 335

<210> 54  
<211> 111  
<212> PRT  
<213> H.Sapiens

<400> 54

Asp His Phe Leu Trp His Pro Gly Glu Tyr Val Phe Phe Ser Ala Gly  
1 5 10 15

Ala Met Lys Ile Arg Asn Asn Pro Val Phe Phe Val Ile Ile Asn Lys  
20 25 30

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Asp Lys Ile Ser Pro Tyr Val Asn Thr Ser Val Met Ser Ser Asn Ser  
35 40 45

Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala Asn Val Asn Gly Ser  
50 55 60

Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile  
65 70 75 80

Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe Gly Asn Leu Leu Val  
85 90 95

Met Ile Ser Ile Leu His Phe Lys Gln Leu His Ser Pro Thr Asn  
100 105 110

<210> 55

<211> 586

<212> DNA

<213> H.Sapiens

<400> 55

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ctattcattc atagtcttac ttgattttta aaaactcatt tcgcttggtta attttaaagg	120
tatcctgaac ttcgtctatc caactgctta tatatgttca gaaaacaaat tcatggttgc	180
tgaactgttc tttaaaacct gaccagttac aataactttt attgctttcc taaaccatgg	240
gtaaaaataaa gcataaatca aaggattcat ggctgagtta taataagcac accaacagca	300
tcataaatac aggcaggggt tataaagccc ataaaggcat caattaatga atcaatgcta	360
tatggtaacc atgaaatcat aaatgctacc actgtgaccc ccagggtttt agctgctttt	420
ctctctctcc tggccactct ggctttgtaa ctctctgagg atgattctgt cttgctacca	480
gtattttcta tctttttcgc ctgtcgtcta gccacaagaa atatgttacc atacagaatt	540
atcataataa aggtaggtat aaagaaggat agaaaatctg tcaaca	586

<210> 56

<211> 190

<212> PRT

<213> H.Sapiens

<400> 56

Leu Thr Asp Phe Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile  
1 5 10 15

Leu Tyr Gly Asn Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile  
20 25 30

Glu Asn Thr Gly Ser Lys Thr Glu Ser Ser Ser Glu Ser Tyr Lys Ala  
35 40 45

Arg Val Ala Arg Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Val Thr

50

55

60

Val Val Ala Phe Met Ile Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu  
65 70 75 80

Ile Asp Ala Phe Met Gly Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile  
85 90 95

Cys Cys Trp Cys Ala Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr  
100 105 110

Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala Ile Lys Val Ile Val Thr  
115 120 125

Gly Gln Val Leu Lys Asn Ser Ser Ala Thr Met Asn Leu Phe Ser Glu  
130 135 140

His Ile Ala Val Gly Thr Lys Phe Arg Ile Pro Leu Lys Leu Pro Ser  
145 150 155 160

Glu Met Ser Phe Lys Ser Ser Lys Thr Met Asn Glu Gln Ile Asn Cys  
165 170 175

Ser Ser Asn Lys Gln Ile Asn Val Phe Gln Ser Cys Asp Val  
180 185 190

<210> 57  
<211> 976  
<212> DNA  
<213> H.Sapiens

<400> 57  
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tggtaggaaa cgggtttgtg ctctggctcc tgggcttccg catgcgcagg aacgccttct 120  
ctgtctacgt cctcagcctg gccggggccg acttctctt cctctgcttc cagattataa 180  
attgcctggt gtacctcagt aacttcttct gttccatctc catcaatttc cctagcttct 240  
tcaccactgt gatgacctgt gcctaccttg caggcctgag catgctgagc accgtcagca 300  
ccgagcgtg cctgtccgtc ctgtggccca tctggtatcg ctgccgccgc ccagacacc 360  
tgtcagcggg cgtgtgtgtc ctgctctggg cctgtccct actgctgagc atcttggaag 420  
ggaagtctg tggcttctta tttagtgatg gtgactctgg ttggtgtcag acatttgatt 480  
tcatcactgc agcgtggctg atttttttat tcatggttct ctgtgggtcc agtctggccc 540  
tgctggtcag gatcctctgt ggctccaggg gtctgccact gaccaggctg tacctgacca 600  
tctgctcac agtgctggtg tccctcctct gggcctgcc ctttggcatt cagtggttcc 660  
taatattatg gatctggaag gattctgatg tcttattttg tcatattcat ccagtttcag 720  
ttgtcctgtc atctcttaac agcagtgcc accccatcat ttacttcttc gtgggctctt 780  
ttaggaagca gtggcggstg cagcaccga tcctcaagct ggctctccag agggctctgc 840

aggacattgc tgaggtggat cacagtgaag gatgcttccg tcagggcacg cggagattca 900  
aagaagcatt ctggtgtagg gatggacccc tctacttcca tcatatatat gtggctttga 960  
gaggcaactt tgcccc 976

<210> 58  
<211> 324  
<212> PRT  
<213> H.Sapiens  
  
<220>  
<221> UNSURE  
<222> (266)..(266)  
<223> Xaa is Unknown

<400> 58

Cys	Gly	Lys	Glu	Thr	Leu	Ile	Pro	Val	Phe	Leu	Ile	Leu	Phe	Ile	Ala	1	5	10	15
Leu	Val	Gly	Leu	Val	Gly	Asn	Gly	Phe	Val	Leu	Trp	Leu	Leu	Gly	Phe	20	25	30	
Arg	Met	Arg	Arg	Asn	Ala	Phe	Ser	Val	Tyr	Val	Leu	Ser	Leu	Ala	Gly	35	40	45	
Ala	Asp	Phe	Leu	Phe	Leu	Cys	Phe	Gln	Ile	Ile	Asn	Cys	Leu	Val	Tyr	50	55	60	
Leu	Ser	Asn	Phe	Phe	Cys	Ser	Ile	Ser	Ile	Asn	Phe	Pro	Ser	Phe	Phe	65	70	75	80
Thr	Thr	Val	Met	Thr	Cys	Ala	Tyr	Leu	Ala	Gly	Leu	Ser	Met	Leu	Ser	85	90	95	
Thr	Val	Ser	Thr	Glu	Arg	Cys	Leu	Ser	Val	Leu	Trp	Pro	Ile	Trp	Tyr	100	105	110	
Arg	Cys	Arg	Arg	Pro	Arg	His	Leu	Ser	Ala	Val	Val	Cys	Val	Leu	Leu	115	120	125	
Trp	Ala	Leu	Ser	Leu	Leu	Leu	Ser	Ile	Leu	Glu	Gly	Lys	Phe	Cys	Gly	130	135	140	
Phe	Leu	Phe	Ser	Asp	Gly	Asp	Ser	Gly	Trp	Cys	Gln	Thr	Phe	Asp	Phe	145	150	155	160
Ile	Thr	Ala	Ala	Trp	Leu	Ile	Phe	Leu	Phe	Met	Val	Leu	Cys	Gly	Ser	165	170	175	
Ser	Leu	Ala	Leu	Leu	Val	Arg	Ile	Leu	Cys	Gly	Ser	Arg	Gly	Leu	Pro	180	185	190	
Leu	Thr	Arg	Leu	Tyr	Leu	Thr	Ile	Leu	Leu	Thr	Val	Leu	Val	Ser	Leu	195	200	205	



Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile  
 210 215 220

Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val  
 225 230 235 240

Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe  
 245 250 255

Val Gly Ser Phe Arg Lys Gln Trp Arg Xaa Gln His Pro Ile Leu Lys  
 260 265 270

Leu Ala Leu Gln Arg Ala Leu Gln Asp Ile Ala Glu Val Asp His Ser  
 275 280 285

Glu Gly Cys Phe Arg Gln Gly Thr Arg Arg Phe Lys Glu Ala Phe Trp  
 290 295 300

Cys Arg Asp Gly Pro Leu Tyr Phe His His Ile Tyr Val Ala Leu Arg  
 305 310 315 320

Gly Asn Phe Ala

<210> 59  
 <211> 578  
 <212> DNA  
 <213> H.Sapiens

<400> 59  
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 gtaacagggt accaaagggtg ttcagagcag cataatgggtc tagaaacgat gtaagcttca 120  
 tggatctgat tctcaatgga acaactgatt gaaagcaggc tgagattcga tcttgaatga 180  
 ccctcaagat atggaagggt aaaaaacata cgtaaaatgc aaggagtagc agaattggtta 240  
 gccttcgtgc tttctgctta aggcagctgt cagtttgagc tccatgggtc aaagtgtgga 300  
 taatcgtggt atagcaaagt gtcactatca ccaaggggag gcagaaagta cttgcagtca 360  
 aaatcagggt gtaccactta atagtattga gttcatccga actggtgagg tcgagacagg 420  
 ctgatctggt ggtcctgttg gttgatgtga tcaagaaggc catcggaatg acagctacca 480  
 gtgaaatgat ccacaccaca gcacaggcta caactgcaca tcgagttttg tgaatggaaa 540  
 agcagctcat tgggtgaatg atcacacagt agcgggaag 578

<210> 60  
 <211> 192  
 <212> PRT  
 <213> H.Sapiens

<400> 60

## 00431PHRM293.ST25

Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His  
 1 5 10 15  
 Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser  
 20 25 30  
 Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg  
 35 40 45  
 Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn  
 50 55 60  
 Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys Leu  
 65 70 75 80  
 Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu  
 85 90 95  
 Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg  
 100 105 110  
 Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro Phe  
 115 120 125  
 His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln Ser  
 130 135 140  
 Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu Asp  
 145 150 155 160  
 His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val  
 165 170 175  
 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys  
 180 185 190

<210> 61  
 <211> 872  
 <212> DNA  
 <213> H.Sapiens

<400> 61  
 gggagggtc gtagacacac taaccctacc ctttctgttt cttcctcatc tttcctttcc 60  
 atctgtttct catggtctcc tgtctgtctc tctctctctc cctctttct ctctcctgc 120  
 tctttctcat cccctccatt tctgtgtcaa tctcaatcca tttatatcgg tggccacttt 180  
 tctatctctt tgttctatct ctctctctct ctctttccca ctttgtctct gcacgcctgt 240  
 tgtgtttttc tgctgtctc tctcttgccc tcctctctct gtctctctct tgccctcatc 300  
 tctctgtctc tctgtgtctg tgtctcccc gctattccc atttgaggt gcaatgtagc 360  
 aggacaactc atggagcccc cccgggcccc tcgagtaccg gactggctga ccccctaggg 420  
 ttggcagtag cccctgaccc tcagtatggc caacactacc ggagagcctg aggaggtgag 480  
 cggcgctctg tccccaccgt ccgcatcagc ttatgtgaag ctggtactgc tgggactgat 540

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tatgtgcgtg agcctggcgg gtaacgccat cttgtccctg ctgggtgctca aggagcgggc 600
cctgcacaag gctccttact acttctctgct ggacctgtgc ctggccgatg gcatacgctc 660
tgccgtctgc ttcccctttg tgctggcttc tgtgcgccac ggctcttcat ggaccttcag 720
tgcaactcagc tgcaagattg tggcctttat ggccgtgctc ttttgcttcc atgcggcctt 780
catgctgttc tgcacacagc tcacccgcta catggccatc gccaccacc gcttctacgc 840
caagcgcgtg acactctgga catgcgcggc tg 872

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<210> 62  
 <211> 143  
 <212> PRT  
 <213> H.Sapiens

<400> 62

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Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1          5          10          15
Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
          20          25          30
Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
          35          40          45
Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
          50          55          60
Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
          65          70          75          80
Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
          85          90          95
Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
          100          105          110
Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
          115          120          125
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Glu
          130          135          140

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<210> 63  
 <211> 962  
 <212> DNA  
 <213> H.Sapiens

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<400> 63
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tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180

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aaacatgaga aggaactgta acctgattat ggatttggga aaaagataaa tcaacacaca      240
aagggaagaa taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat      300
taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt      360
aatggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatatc      420
acacttcaaa caacttcata ccccaacaaa ttgggtcatt cattccatgg ccactgtgga      480
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gtatttttga gaagtcttct gtaaaaattca cacaagcacc gacattatgc tgagctcagc      600
ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact      660
gagatataaa gccaagatga atatcttggt tatttgtgtg atgatcttca ttagttggag      720
tgtccctgct gtttttgcac ttggaatgat ctttctggag ctaaaacttca aaggcgctga      780
agagatatat tacaacatg ttcactgcag aggaggttgc tctgtcttct ttagcaaaat      840
atctggggta ctgaccttta tgacttcttt ttatatacct ggatctatta tgttatgtgt      900
ctattacaga atatcttta tcgctaaaga acaggcaaga ttaattagtg atgccaatca      960
ga

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<210> 64
<211> 238
<212> PRT
<213> H.Sapiens

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<400> 64

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Arg Glu Lys Thr Asp Gln Pro Ser Gly Met Met Pro Phe Cys His Asn
1          5          10          15
Ile Ile Asn Ile Ser Cys Val Lys Asn Asn Trp Ser Asn Asp Val Arg
20          25          30
Ala Ser Leu Tyr Ser Leu Met Val Leu Ile Ile Leu Thr Thr Leu Val
35          40          45
Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu His
50          55          60
Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe Leu
65          70          75          80
Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu His
85          90          95
Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr Asp
100         105         110
Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser Ile

```

115

120

125

Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys Met  
 130 135 140

Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val Pro  
 145 150 155 160

Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys Gly  
 165 170 175

Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys Ser  
 180 185 190

Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser Phe  
 195 200 205

Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr Leu  
 210 215 220

Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln  
 225 230 235

<210> 65  
 <211> 1018  
 <212> DNA  
 <213> H.Sapiens

<400> 65  
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 aagaaccaat gtcttgctca gatagaagca agatactcag acttagtttc tctgtagctc 120  
 ctgcttttta ttattcctgg ttggattgca ccactactca gtttctatgt tataatactg 180  
 attataaaac atgggagggg aataactttg tattggtttt tatggataat ttattatgtg 240  
 tcctagactc tggccttgctc aaaagaagga cgtaagaagg cacgatgtat tatacttggg 300  
 aatgatagaa gagactgacc tggatatttc acccggaaga gggaaaaggat tttaactaca 360  
 aatacaggaa tccagcagat ggcacagag aacactataa aaaagaaacg atttgcaaca 420  
 gccacctctc ttccaaaaca attccttact tctgtggtct gcaaggcggg tttttgaatg 480  
 gaacagaaca tagtaataata ggaaaacaca atgatgagaa aagccagcaa gttcacacct 540  
 gttggggaaa agcacacttt taacatctca ggcgtaaaaag tcaacagtaa aattactgtg 600  
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 caaaatttat ttatgtttca tatacacctt atacacatag tctgaaagta attttgtaca 780  
 atattttaaa taattttggg catgaaacaa agtttgcata cattgaacca tcagacagca 840  
 aaagcttcag gtgtggaatt ttccacttgt ggcacatgt tgatgctcaa aaagttccat 900

attttagagc atttcaaatt ttggattttc aaattacaaa tgcttaacct gtacttagat 960

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<210> 66  
 <211> 327  
 <212> PRT  
 <213> H.Sapiens

<400> 66

Tyr	Ile	Lys	Glu	Cys	Phe	Leu	Lys	Val	Pro	Val	Glu	Glu	Ala	Leu	Tyr	1	5	10	15
Leu	Thr	Ser	Lys	Tyr	Arg	Leu	Ser	Ile	Cys	Asn	Leu	Lys	Ile	Gln	Asn	20	25	30	
Leu	Lys	Cys	Ser	Lys	Ile	Trp	Asn	Phe	Leu	Ser	Ile	Asn	Met	Met	Pro	35	40	45	
Gln	Val	Glu	Asn	Ser	Thr	Pro	Glu	Ala	Phe	Ala	Val	Trp	Phe	Asn	Val	50	55	60	
Cys	Lys	Leu	Cys	Phe	Met	Pro	Lys	Ile	Ile	Asn	Ile	Val	Gln	Asn	Tyr	65	70	75	80
Phe	Gln	Thr	Met	Cys	Ile	Arg	Cys	Ile	Asn	Ile	Asn	Lys	Phe	Cys	Val	85	90	95	
Thr	Trp	Glu	Pro	Phe	Pro	Arg	Tyr	Ile	Ile	Met	Asn	Val	Ile	Phe	Arg	100	105	110	
Asn	Pro	Lys	Ser	Lys	Thr	Phe	Leu	Val	Ser	Asn	Ile	Leu	Gly	Lys	Gly	115	120	125	
Tyr	Ser	Thr	Cys	Thr	Thr	Val	Ile	Leu	Leu	Leu	Thr	Phe	Thr	Pro	Glu	130	135	140	
Met	Leu	Lys	Val	Cys	Phe	Ser	Pro	Thr	Gly	Val	Asn	Leu	Leu	Ala	Phe	145	150	155	160
Leu	Ile	Ile	Val	Phe	Ser	Tyr	Ile	Thr	Met	Phe	Cys	Ser	Ile	Gln	Lys	165	170	175	
Thr	Ala	Leu	Gln	Thr	Thr	Glu	Val	Arg	Asn	Cys	Phe	Gly	Arg	Glu	Val	180	185	190	
Ala	Val	Ala	Asn	Arg	Phe	Phe	Phe	Ile	Val	Phe	Ser	Asp	Ala	Ile	Cys	195	200	205	
Trp	Ile	Pro	Val	Phe	Val	Val	Lys	Ile	Leu	Ser	Leu	Phe	Arg	Val	Glu	210	215	220	
Ile	Pro	Gly	Gln	Ser	Leu	Leu	Ser	Phe	Pro	Ser	Ile	Ile	His	Arg	Ala	225	230	235	240
Phe	Leu	Arg	Pro	Ser	Phe	Asp	Lys	Ala	Arg	Val	Asp	Thr	Ile	Ile	His	245	250	255	

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Lys Asn Gln Tyr Lys Val Ile Ser Leu Pro Cys Phe Ile Ile Ser Ile  
260 265 270

Ile Lys Lys Leu Ser Ser Gly Ala Ile Gln Pro Gly Ile Ile Lys Ser  
275 280 285

Arg Ser Tyr Arg Glu Thr Lys Ser Glu Tyr Leu Ala Ser Ile Ala Arg  
290 295 300

His Trp Phe Phe Thr Arg Ser Met His Lys Thr Ile Lys Ile Tyr Met  
305 310 315 320

Pro Arg Phe His Pro Gly Leu  
325

<210> 67

<211> 1251

<212> DNA

<213> H.Sapiens

<400> 67

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ggcacgcgtc tggcgtgct cctgctcagc ctggccctct ctgacttctt gttcctggca      240
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cgcccagtcg gcctgcccct ctgggtctgc gccggtgtct gggctgtggc cacactcttc      480
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cggaccctgc tgcgctccgt gctctcgtcc ttcgcggcag ctctctgcga ggagcggccg      960
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<210> 68  
 <211> 417  
 <212> PRT  
 <213> H.Sapiens  
 <400> 68

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Glu	Leu	Asp	Asp	Glu	Asp	Ser	Tyr	Pro	Gln	Gly	Gly	Trp	Asp	Thr	Val
			20					25					30		
Phe	Leu	Val	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Pro	Ala	Asn	Gly	Leu	Met
		35					40					45			
Ala	Trp	Leu	Ala	Gly	Ser	Gln	Ala	Arg	His	Gly	Ala	Gly	Thr	Arg	Leu
	50					55					60				
Ala	Leu	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Ser	Asp	Phe	Leu	Phe	Leu	Ala
65					70					75					80
Ala	Ala	Ala	Phe	Gln	Ile	Leu	Glu	Ile	Arg	His	Gly	Gly	His	Trp	Pro
				85					90					95	
Leu	Gly	Thr	Ala	Ala	Cys	Arg	Phe	Tyr	Tyr	Phe	Leu	Trp	Gly	Val	Ser
			100					105					110		
Tyr	Ser	Ser	Gly	Leu	Phe	Leu	Leu	Ala	Ala	Leu	Ser	Leu	Asp	Arg	Cys
		115					120						125		
Leu	Leu	Ala	Leu	Cys	Pro	His	Trp	Tyr	Pro	Gly	His	Arg	Pro	Val	Arg
	130					135					140				
Leu	Pro	Leu	Trp	Val	Cys	Ala	Gly	Val	Trp	Val	Leu	Ala	Thr	Leu	Phe
145				150						155					160
Ser	Val	Pro	Trp	Leu	Val	Phe	Pro	Glu	Ala	Ala	Val	Trp	Trp	Tyr	Asp
				165					170					175	
Leu	Val	Ile	Cys	Leu	Asp	Phe	Trp	Asp	Ser	Glu	Glu	Leu	Ser	Leu	Arg
			180					185					190		
Met	Leu	Glu	Val	Leu	Gly	Gly	Phe	Leu	Pro	Phe	Leu	Leu	Leu	Leu	Val
		195					200					205			
Cys	His	Val	Leu	Thr	Gln	Ala	Thr	Ala	Cys	Arg	Thr	Cys	His	Arg	Gln
	210					215					220				
Gln	Gln	Pro	Ala	Ala	Cys	Arg	Gly	Phe	Ala	Arg	Val	Ala	Arg	Thr	Ile
225					230					235					240
Leu	Ser	Ala	Tyr	Val	Val	Leu	Arg	Leu	Pro	Tyr	Gln	Leu	Ala	Gln	Leu



245

250

255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp  
 260 265 270

Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu  
 275 280 285

Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu  
 290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro  
 305 310 315 320

Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly  
 325 330 335

Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro  
 340 345 350

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
 355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
 370 375 380

Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
 385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
 405 410 415

Ala

<210> 69  
 <211> 659  
 <212> DNA  
 <213> H.Sapiens

<400> 69  
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 ccctgtccct gctgcagagc atcctggaat ggatgttctg tggcttcctg tctagtgggtg 180  
 ctgattctgt ttggtgtgaa acatcagatt tcatcacagt cacatggctg atttttttat 240  
 gtgtggttct ctgcgggtcc agcccggttc tgctggtcag gatcctttgt ggatcccgga 300  
 agatgccctt gaccaggctg tacatgacca tcctgctcag agtgctggtc ttctctctct 360  
 gtgacctgcc ctttggcatt cagtgattcc tatttttctg gatccacgtg gatttgtcac 420  
 gttcgtctag tttccatttt cctgtccact cttaacagca gtgccaaccc cattattttac 480  
 ttcttcatgg gctcctttag gcagcttcaa aacaggaaga ctctctagct gggttctccag 540

aggggctctgc aggacacgcc tgagggtggaa gaaggcagat ggcggctttc tgaggaaacc 600  
 ctggagctgt catgaagcag attggggcca tgaggaagag cctctgccct gtcagtcag 659

<210> 70  
 <211> 213  
 <212> PRT  
 <213> H.Sapiens

<400> 70

Tyr Arg Pro Glu His Ala Gly Leu His Gln His Gln Ala Leu Pro Val  
 1 5 10 15  
 His Pro Val Ala His Leu Val Pro Leu Pro Pro Pro His Thr Pro Val  
 20 25 30  
 Ser Ser Arg Val Ser Cys Ser Gly Pro Cys Pro Cys Cys Arg Ala Ser  
 35 40 45  
 Trp Asn Gly Cys Ser Val Ala Ser Cys Leu Val Val Leu Ile Leu Phe  
 50 55 60  
 Gly Val Lys His Gln Ile Ser Ser Gln Ser His Gly Phe Phe Tyr Val  
 65 70 75 80  
 Trp Phe Ser Ala Gly Pro Ala Arg Phe Cys Trp Ser Gly Ser Phe Val  
 85 90 95  
 Asp Pro Gly Arg Cys Pro Pro Gly Cys Thr Pro Ser Cys Ser Glu Cys  
 100 105 110  
 Trp Ser Ser Ser Ser Val Thr Cys Pro Leu Ala Phe Ser Asp Ser Tyr  
 115 120 125  
 Phe Ser Gly Ser Thr Trp Ile Cys His Val Arg Leu Val Ser Ile Phe  
 130 135 140  
 Leu Ser Thr Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met  
 145 150 155 160  
 Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Leu Val Leu Gln  
 165 170 175  
 Arg Ala Leu Gln Asp Thr Pro Glu Val Glu Glu Gly Arg Trp Arg Leu  
 180 185 190  
 Ser Glu Glu Thr Leu Glu Leu Ser Ser Arg Leu Gly Pro Gly Arg Ala  
 195 200 205  
 Ser Ala Leu Ser Val  
 210

<210> 71  
 <211> 559  
 <212> DNA  
 <213> H.Sapiens

<400> 71  
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 cccacacatg gtgcaacaca gcagagccag cagcaccgct gccaccagcc acagcgtccg 180  
 gcacaagtgg cggctgggct ccccgaagaa ctgggtgcag gcgccgctga gcagcaggtg 240  
 cagcagcagg cagagggccc aggtgagggc gcacacacag gtggtcaggt ggcgtgggcg 300  
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 caggagactc agggccacga tgtagcagaa gaagcgcagc gttgccaggc tggctgcac 420  
 gaagcccggg aagtccagcc ggccttgcat caagtcgggg acgatggcca ccatgtggca 480  
 gccaaaggaag atgagatccg cgcaggccac gtccaggagg tagatggcga aagggtttct 540  
 gtagacattg gagctgagc 559

<210> 72  
 <211> 211  
 <212> PRT  
 <213> H.Sapiens

<400> 72  
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 Val Ala Cys Ala Asp Leu Ile Phe Leu Gly Cys His Met Val Ala Ile  
 20 25 30  
 Val Pro Asp Leu Leu Gln Gly Arg Leu Asp Phe Pro Gly Phe Val Gln  
 35 40 45  
 Thr Ser Leu Ala Thr Leu Arg Phe Phe Cys Tyr Ile Val Gly Leu Ser  
 50 55 60  
 Leu Leu Ala Ala Val Ser Val Glu Gln Cys Leu Ala Ala Leu Phe Pro  
 65 70 75 80  
 Ala Trp Tyr Ser Cys Arg Arg Pro Arg His Leu Thr Thr Cys Val Cys  
 85 90 95  
 Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Thr Thr Cys Val  
 100 105 110  
 Cys Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Leu Leu Ser  
 115 120 125  
 Gly Ala Cys Thr Leu Leu Leu Ser Gly Ala Cys Thr Gln Phe Phe Gly  
 130 135 140  
 Glu Pro Ser Arg His Leu Cys Arg Thr Leu Trp Leu Val Ala Ala Val  
 145 150 155 160

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Leu Leu Ala Leu Leu Cys Cys Thr Met Cys Gly Ala Ser Leu Met Leu  
 165 170 175

Leu Leu Arg Val Glu Arg Gly Pro Gln Arg Pro Pro Pro Arg Gly Phe  
 180 185 190

Pro Gly Leu Ile Leu Leu Thr Val Leu Leu Phe Ser Ser Ala Ala Cys  
 195 200 205

Leu Arg His  
 210

<210> 73  
 <211> 1008  
 <212> DNA  
 <213> H.Sapiens

<400> 73  
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 ctctgcttca ccttgaatct ggctgtggct gacaccttga ttggtgtggc catctctggc 180  
 ctactcacag accagctctc cagcccttct cggcccacac agaagaccct gtgcagcctg 240  
 cggatggcat ttgtcacttc ctccgcagct gcctctgtcc tcacggatcat gctgatcacc 300  
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 aagatggaac atgcaggagc catggctgga ggttatcgat cccacaggac tcccagcgac 660  
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 ctcacctcat tctcctctt tctctcgcc aggaattgtg gccagagag gccagggaa 960  
 agttcctgtc acatcgtcac tatctccagc tcagagtttg atggctaa 1008

<210> 74  
 <211> 335  
 <212> PRT  
 <213> H.Sapiens

<400> 74

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser  
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 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu  
 20 25 30  
 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala  
 35 40 45  
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp  
 50 55 60  
 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu  
 65 70 75 80  
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val  
 85 90 95  
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg  
 100 105 110  
 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly  
 115 120 125  
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro  
 130 135 140  
 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val  
 145 150 155 160  
 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro  
 165 170 175  
 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala  
 180 185 190  
 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met  
 195 200 205  
 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu  
 210 215 220  
 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro  
 225 230 235 240  
 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu  
 245 250 255  
 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
 260 265 270  
 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu  
 275 280 285  
 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
 290 295 300  
 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu

305

310

315

320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
 325 330 335

&lt;210&gt; 75

&lt;211&gt; 2137

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 75

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cttccctca cacacacacc ccctcgtgc cgaattc 2137

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<210> 76
<211> 359
<212> PRT
<213> H.Sapiens

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<400> 76

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Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
          20          25          30
Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
          35          40          45
Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
50          55          60
Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
65          70          75          80
Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
          85          90          95
Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
          100          105          110
Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
          115          120          125
Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
130          135          140

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Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg  
 145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
 165 170 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
 180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
 195 200 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
 210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala  
 225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
 245 250 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
 260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
 275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
 290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
 305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
 325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu  
 340 345 350

Gln Arg Gln Glu Ser Val Phe  
 355

<210> 77  
 <211> 1197  
 <212> DNA  
 <213> H.Sapiens

<400> 77  
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 gtggtgtgcc tggcgggtgtg cgccttcacg gtgctagaga atctagccgt gttgttggtg 180  
 ctcggaacgcc acccgcgctt ccacgctccc atgttcctgc tctgggcag cctcacgttg 240  
 tcggatctgc tggcaggcgc cgcctacgcc gccaacatcc tactgtcggg gccgctcacg 300  
 ctgaaactgt cccccgcgct ctggttcgca cgggaggag gcgtcttcgt ggcactcact 360



gcgtccgtgc tgagcctcct ggccatcgcg ctggagcgca gcctcaccat ggcgcgcagg 420  
 gggcccgcg ccgtctccag tcggggggcg acgctggcga tggcagccgc ggcctggggc 480  
 gtgtcgctgc tctcggggct cctgccagcg ctgggctgga attgcctggg tcgcctggac 540  
 gcttgctcca ctgtcttgcc gctctacgcc aaggcctacg tgctcttctg cgtgctcgcc 600  
 ttctgtggga tcttgccgc tatctgtgca ctctacgcgc gcctctactg ccaggtagcg 660  
 gccaacgcgc ggcgcctgcc ggcacggccc gggactgcgg ggaccacctc gaccggggcg 720  
 cgtcgcaagc cgcgctcgct ggccttgctg cgcacgctca gcgtgggtgct cctggccttt 780  
 gtggcatgtt gggggccctt cttcctgctg ctgttgctcg acgtggcgtg cccggcgcg 840  
 acctgtcctg tactcctgca ggccgatccc ttctggggac tggccatggc caactcactt 900  
 ctgaacccca tcctctacac gctcaccaac cgcgacctgc gccacgcgct cctgcgcctg 960  
 gtctgctgcg gacgccactc ctgcggcaga gaccgagtg gctcccagca gtcggcgagc 1020  
 gcggctgagg cttccggggg cctgcgcgcg tgccctgccc cgggccttga tgggagcttc 1080  
 agcggctcgg agcgtctatc gcccagcgcg gacgggctgg acaccagcgg ctccacaggc 1140  
 agccccggtg caccacagc cgcccgact ctggtatcag aaccggctgc agactga 1197

<210> 78  
 <211> 398  
 <212> PRT  
 <213> H.Sapiens

<400> 78

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val  
 1 5 10 15  
 Leu His Tyr Asn Tyr, Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro  
 20 25 30  
 Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala  
 35 40 45  
 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His  
 50 55 60  
 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu  
 65 70 75 80  
 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser  
 85 90 95  
 Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu  
 100 105 110  
 Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala

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115

120

125

Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro  
 130 135 140

Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly  
 145 150 155 160

Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu  
 165 170 175

Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala  
 180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile  
 195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg  
 210 215 220

Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala  
 225 230 235 240

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val  
 245 250 255

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu  
 260 265 270

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala  
 275 280 285

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile  
 290 295 300

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu  
 305 310 315 320

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln  
 325 330 335

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu  
 340 345 350

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro  
 355 360 365

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala  
 370 375 380

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp  
 385 390 395

&lt;210&gt; 79

&lt;211&gt; 1041

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 79

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atgtacaacg ggtcgtgctg ccgcatcgag ggggacacca tctcccaggt gatgccgccg      60
ctgctcattg tggcctttgt gctgggcgca ctaggcaatg gggtcgccct gtgtggtttc      120
tgcttcaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct      180
gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac      240
tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc      300
gggagcatcg tgttccttac ggtgggtggct gcggacaggt atttcaaagt ggtccacccc      360
caccacgcgg tgaacactat ctccaccggg gtggcggtcg gcatcgtctg caccctgtgg      420
gccctgggtca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag      480
acggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg      540
ttccagctgg agttctttat gccctcggc atcatcttat tttgctcctt caagattggt      600
tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgacccgg      660
ttcatcatgg tgggtggcaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga      720
ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg      780
cacataaacc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatttt      840
tcaagcccct cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag      900
cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc      960
aggagtgcga tcagtgtggc aaatagtttc caaagccagt ctgatgggca atgggatccc     1020
cacattgttg agtggcactg a                                           1041

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<210> 80  
 <211> 346  
 <212> PRT  
 <213> H.Sapiens

<400> 80

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Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
1          5          10          15
Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
          20          25          30
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
          35          40          45
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
          50          55          60
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65          70          75          80

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## 00431PHRM293.ST25

Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala  
 85 90 95  
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp  
 100 105 110  
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser  
 115 120 125  
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile  
 130 135 140  
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu  
 145 150 155 160  
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp  
 165 170 175  
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile  
 180 185 190  
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln  
 195 200 205  
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val  
 210 215 220  
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg  
 225 230 235 240  
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val  
 245 250 255  
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
 260 265 270  
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe  
 275 280 285  
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His  
 290 295 300  
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg  
 305 310 315 320  
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly  
 325 330 335  
 Gln Trp Asp Pro His Ile Val Glu Trp His  
 340 345

<210> 81  
 <211> 2525  
 <212> DNA  
 <213> H.Sapiens

<400> 81  
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60

gcgacccctat agtgacaccc cacttaataca gcctctactt catagtgcctt attggcgggc 120  
 tgggtgggtgt catttccatt cttttcctcc tgggtgaaaat gaacaccccg tcaagtgacca 180  
 ccatggcgggt cattaacttg gtgggtgggcc acagcgtttt tctgctgaca gtgccatttc 240  
 gcttgaccta cctcatcaag aagacttgga tgtttgggct gcccttctgc aaatttgtga 300  
 gtgccatgct gcacatccac atgtacctca cgttcctatt ctatgtgggtg atcctgggtca 360  
 ccagatacct catcttcttc aagtgcaaag acaaagtgga attctacaga aaactgcatg 420  
 ctgtggctgc cagtgcctggc atgtggacgc tgggtgattgt cattgtggta cccctgggtg 480  
 tctcccggtg tggaatccat gaggaatata atgaggagca ctgtttttaa tttcaciaaag 540  
 agcttgctta cacatatgtg aaaatcatca actatatgat agtcattttt gtcatagccg 600  
 ttgctgtgat tctgttggtc ttccaggtct tcatcattat gttgatgggtg cagaagctac 660  
 gccactcttt actatccac caggagttct gggctcagct gaaaaaccta ttttttatag 720  
 gggtcacctt tgtttgtttc cttccctacc agttcttttag gatctattac ttgaatgttg 780  
 tgacgcattc caatgcctgt aacagcaagg ttgcatttta taacgaaatc ttcttgagtg 840  
 taacagcaat tagctgctat gatttgcttc tctttgtctt tgggggaagc cattggttta 900  
 agcaaaagat aattggctta tggaattgtg ttttgtgccg ttagccacaa actacagtat 960  
 tcatatttgc ttcctttata ttgggaataa aaatgggtat aggggaggta agaatggtat 1020  
 ttcattactt gatcaaaacc atgccttgat gtacccaaaa caaaaggact ataaaatgca 1080  
 agagccctca ttgtagtcct tatgggatcc ctcccatctc tgagtgatgg ccgtacaaaag 1140  
 accagtgttg ttgaatccac ctggagttgc aatattacat tattttccag tacagaatgt 1200  
 ctgtgtggcc catgaaagca acatagggtt taagagtttt agagtttcat tagctcattc 1260  
 taagtctctc tgtttgaagc atgggtctctt aggttttgga ctgaactcag acctttagtt 1320  
 cttttcatcc cacttcacct taggtaagta aattctggcc accaccagc tccaaagaca 1380  
 caaactctcc ttcgctaacc aggttagatg tccattcat ctcatgcctt gataaaaact 1440  
 gataagggga gagaatagtt aaaaattttt ctagggtatc ataactctgg taggaagtca 1500  
 tctgtctaga aatcaagaga aaaagaacgt gtggcctcct gttataacaa gggtttctag 1560  
 atttgtcctg tgaaaggctg tttaaggact tggggatcaa cttcctcaat tatcaccaat 1620  
 tgcactgttg ctccaaaaat catttaaaag cttactggac atatctacat aatggtgaaa 1680  
 ctgtaattta gagactatcc ctgactaatg tgctggtagg cattaaaatg agttcccaag 1740  
 ggaagtgatt aaaatttttt tctcttctgt tttttgagag aatttctaga tgtcctgggc 1800  
 cacagttaat taagattttt aggggggaca gaaagttata ctgaaatctt tagagctccc 1860

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ttccgccggtt aaaattatat atatatatat ttaaattata ccttaagttc tgggggtacat 1920
gtgcagaatg tgcaggtttg ttacataggt atacacgtgc catggtgggt tgcggcacct 1980
gtcaacccat ctacattagg tattttctct aatgctctcc ctcccctagc cccccacccc 2040
tggaacaggcc ccattgtgtg atgttcccct ccctgtgtcc atgtgttttc attgttcaac 2100
tcccacttct aagtgagaac atgcggtggt tggttttctg ttctgtgtt agtttgctga 2160
gaatgatggt ttccagggtt aaattatata tttttaaata aatgaaaact gtgtttttta 2220
aagaggactt ttgagaagta tatagaaaaa ccattaattt agactctgtg agattaggtt 2280
gcatgaagaa ggtttttctga atatttgaag agtggataaa taaatgtccc ccaaagcaat 2340
aaaatcataa tcctttaaaaa tataggaaaa ataactaatg ggaactaggc ttaataactg 2400
ggatgaaata atctgtacaa caaactccca tgacacatgt ttacctatgt aacaaacctg 2460
cacatgtacc cctgaactta aaataaaaatt taaagtataa taataaaata atatggattt 2520
tctttt 2525

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<210> 82
<211> 312
<212> PRT
<213> H.Sapiens

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<400> 82

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Met Thr Gly Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg Asn
1          5          10          15
Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe
20          25          30
Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu
35          40          45
Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn
50          55          60
Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu
65          70          75          80
Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys
85          90          95
Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe
100         105         110
Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys
115         120         125
Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala
130         135         140

```

Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val Ser  
145 150 155 160

Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe  
165 170 175

His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile  
180 185 190

Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val  
195 200 205

Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser  
210 215 220

His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val  
225 230 235 240

Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu  
245 250 255

Asn Val Val Thr His Ser Asn Ala Cys Asn Ser Lys Val Ala Phe Tyr  
260 265 270

Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu Leu  
275 280 285

Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile Gly  
290 295 300

Leu Trp Asn Cys Val Leu Cys Arg  
305 310

<210> 83  
<211> 1125  
<212> DNA  
<213> H.Sapiens

<400> 83  
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acttctccat atgtaaaataa cagcggttatg agcagcaatt catccctgct ggtggctgtg 120  
cagctgtgct acgcgaacgt gaatgggtcc tgtgtgaaaa tccccttctc gccgggatcc 180  
cgggtgattc tgtacatagt gtttggtttt ggggctgtgc tggctgtgtt tggaaacctc 240  
ctggtgatga tttcaatcct ccatttcaag cagctgcact ctccgaccaa ttttctcggt 300  
gcctctctgg cctgcgctga tttcttggtg ggtgtgactg tgatgccctt cagcatggtc 360  
aggacggtgg agagctgctg gtattttggg aggagttttt gtactttcca cacctgctgt 420  
gatgtggcat tttgttactc ttctctcttt cacttgctgt tcatctccat cgacaggtac 480  
attgcggtta ctgaccccct ggtctatcct accaagttca ccgtatctgt gtcaggaatt 540  
tgcatcagcg tgtcctggat cctgcccctc atgtacagcg gtgctgtgtt ctacacaggt 600

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gtctatgacg atgggctgga ggaattatct gatgccctaa actgtatagg aggttgtcag      660
accgttgtaa atcaaaactg ggtgttgaca gattttctat ctttctttat acctaccttt      720
attatgataa ttctgtatgg taacatattt cttgtggcta gacgacaggc gaaaaagata      780
gaaaatactg gtagcaagac agaatcatcc tcagagagtt acaaagccag agtggccagg      840
agagagagaa aagcagctaa aaccctgggg gtcacagtgg tagcatttat gatttcattg      900
ttaccatata gcattgattc attaattgat gcctttatgg gctttataac ccctgcctgt      960
atztatgaga tttgctgttg gtgtgcttat tataactcag ccatgaatcc tttgatttat     1020
gctttatttt acccatggtt taggaaagca ataaaagtta ttgtaactgg tcaggtttta     1080
aagaacagtt cagcaacat gaatttgttt tctgaacata tataa                        1125

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<210> 84
<211> 345
<212> PRT
<213> H.Sapiens

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<400> 84

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Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
1          5          10          15
Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
          20          25          30
Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
          35          40          45
Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
          50          55          60
Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
65          70          75          80
Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
          85          90          95
Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
          100          105          110
Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
          115          120          125
Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
          130          135          140
Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
145          150          155          160
Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly
          165          170          175

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## 00431PHRM293.ST25

Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr  
 180 185 190  
 Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile  
 195 200 205  
 Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala  
 210 215 220  
 Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser  
 225 230 235 240  
 Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala  
 245 250 255  
 Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile Ser Trp Leu  
 260 265 270  
 Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr  
 275 280 285  
 Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser  
 290 295 300  
 Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys  
 305 310 315 320  
 Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala  
 325 330 335  
 Thr Met Asn Leu Phe Ser Glu His Ile  
 340 345

<210> 85  
 <211> 1020  
 <212> DNA  
 <213> H.Sapiens

<400> 85  
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 gcttttggaa attgcactga tgaaaacatc ccactcaaga tgcactacct ccctgttatt 120  
 tatggcatta tcttcctcgt gggatttcca ggcaatgcag tagtgatata cacttacatt 180  
 ttcaaaatga gaccttggaa gagcagcacc atcattatgc tgaacctggc ctgcacagat 240  
 ctgctgtatc tgaccagcct ccccttcctg attcactact atgccagtgg cgaaaactgg 300  
 atctttggag atttcatgtg taagtttatc cgcttcagct tccatttcaa cctgtatagc 360  
 agcatcctct tcctcacctg tttcagcatc ttccgctact gtgtgatcat tcaccaatg 420  
 agctgctttt ccattcacia aactcgatgt gcagttgtag cctgtgctgt ggtgtggatc 480  
 atttactggt tagctgtcat tccgatgacc ttcttgatca catcaaccaa caggaccaac 540  
 agatcagcct gtctcgacct caccagttcg gatgaactca atactattaa gtggtacaac 600

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ctgattttga ctgcaagtac tttctgcctc cccttggtga tagtgacact ttgctataacc 660
acgattatcc acactttgac ccatggactg caaactgaca gctgccttaa gcagaaagca 720
cgaaggctaa ccattctgct actccttgca ttttacgtat gttttttacc cttccatatac 780
ttgagggtca ttcaggatcg aatctcagcc tgctttcaat cagttgttcc attgagaatc 840
agatccatga agcttacatc gtttctagac cattatgctg ctctgaacac ctttggtaac 900
ctgttactat atgtggtggt cagcgacaac tttcagcagg ctgtctgctc aacagtgaga 960
tgcaaagtaa gcgggaacct tgagcaagca aagaaaatta gttactcaaa caacccttga 1020

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<210> 86  
 <211> 336  
 <212> PRT  
 <213> H.Sapiens

<400> 86

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Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp
1          5          10          15
Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
          20          25          30
Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
          35          40          45
Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
          50          55          60
Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
65          70          75          80
Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
          85          90          95
Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
          100          105          110
Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
          115          120          125
Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
          130          135          140
His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
145          150          155          160
Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
          165          170          175
Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
          180          185          190

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Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys  
195 200 205

Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr  
210 215 220

Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg  
225 230 235 240

Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro  
245 250 255

Phe His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln  
260 265 270

Ser Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu  
275 280 285

Asp His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val  
290 295 300

Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys  
305 310 315 320

Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn  
325 330 335

<210> 87

<211> 1138

<212> DNA

<213> H.Sapiens

<400> 87

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aagggaaaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat      300
taatatttcc tgtgtgaaaa acaactgggtc aaatgatgtc cgtgcttccc tgtacagttt      360
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## 00431PHRM293.ST25

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile  
210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly  
225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val  
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val  
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Ala  
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Arg Gly Ser Arg Ala Asn Ser Ala  
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<210> 89

<211> 1023

<212> DNA

<213> H.Sapiens

<400> 89

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tggctcattc attccatggc cactgtggac tttcttctgg ggtgtctggt catgccttac 240  
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caggcaagat taattagtga tgccaatcag aagctccaaa ttggattgga aatgaaaaat 720  
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<210> 90  
 <211> 339  
 <212> PRT  
 <213> H.Sapiens

<400> 90

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			20					25					30		
Ile	Ile	Leu	Thr	Thr	Leu	Val	Gly	Asn	Leu	Ile	Val	Ile	Val	Ser	Ile
		35					40					45			
Ser	His	Phe	Lys	Gln	Leu	His	Thr	Pro	Thr	Asn	Trp	Leu	Ile	His	Ser
	50					55					60				
Met	Ala	Thr	Val	Asp	Phe	Leu	Leu	Gly	Cys	Leu	Val	Met	Pro	Tyr	Ser
65					70					75					80
Met	Val	Arg	Ser	Ala	Glu	His	Cys	Trp	Tyr	Phe	Gly	Glu	Val	Phe	Cys
				85					90					95	
Lys	Ile	His	Thr	Ser	Thr	Asp	Ile	Met	Leu	Ser	Ser	Ala	Ser	Ile	Phe
			100					105					110		
His	Leu	Ser	Phe	Ile	Ser	Ile	Asp	Arg	Tyr	Tyr	Ala	Val	Cys	Asp	Pro
	115						120					125			
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	130					135					140				
Phe	Ile	Ser	Trp	Ser	Val	Pro	Ala	Val	Phe	Ala	Phe	Gly	Met	Ile	Phe
145					150					155					160
Leu	Glu	Leu	Asn	Phe	Lys	Gly	Ala	Glu	Glu	Ile	Tyr	Tyr	Lys	His	Val
				165					170					175	
His	Cys	Arg	Gly	Gly	Cys	Ser	Val	Phe	Phe	Ser	Lys	Ile	Ser	Gly	Val
			180					185					190		
Leu	Thr	Phe	Met	Thr	Ser	Phe	Tyr	Ile	Pro	Gly	Ser	Ile	Met	Leu	Cys
		195					200					205			
Val	Tyr	Tyr	Arg	Ile	Tyr	Leu	Ile	Ala	Lys	Glu	Gln	Ala	Arg	Leu	Ile
	210					215					220				
Ser	Asp	Ala	Asn	Gln	Lys	Leu	Gln	Ile	Gly	Leu	Glu	Met	Lys	Asn	Gly
225					230					235					240
Ile	Ser	Gln	Ser	Lys	Glu	Arg	Lys	Ala	Val	Lys	Thr	Leu	Gly	Ile	Val
				245					250					255	
Met	Gly	Val	Phe	Leu	Ile	Cys	Trp	Cys	Pro	Phe	Phe	Ile	Cys	Thr	Val
			260					265					270		

## 00431PHRM293.ST25

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val  
 275 280 285

Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr  
 290 295 300

Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe  
 305 310 315 320

Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu  
 325 330 335

Leu Ser Ser

<210> 91  
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 <212> DNA  
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 cacagcaccg tctctcccat actcggatcat tcacaccatc attgattcac caggcaccac 180  
 tccgtgtcca gcaggactct ggggacccca aatggacact accatggaag ctgacctggg 240  
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 ctgggacacg gtcttctctg tggccctgct gctccttggg ctgccagcca atgggttgat 360  
 ggcgtggctg gccggctccc aggcccgga tggagctggc acgcgtcttg cgctgctcct 420  
 gctcagcctg gccctctctg acttcttgtt cctggcagca gcggccttcc agatcctaga 480  
 gatccggcat gggggacact ggccgctggg gacagctgcc tgccgcttct actacttct 540  
 atggggcgtg tctactcct ccggcctctt cctgctggcc gccctcagcc tcgaccgctg 600  
 cctgctggcg ctgtgcccac actggtaccc tgggcaccgc ccagtcgcc tgcccctctg 660  
 ggtctgcgcc ggtgtctggg tgctggccac actcttcagc gtgccctggc tgggtcttccc 720  
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 gctgtcgtg aggatgctgg aggtcctggg gggcttctct ccttctctcc tgctgctcgt 840  
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 ctacctgctc tgggaggccc tgggtctact cgactacctg atcctactca acagctgcct 1080  
 cagccccttc ctctgcctca tggccagtgc cgacctccgg accctgctgc gctccgtgct 1140

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cccaacccca tctctgcac ctaccccagg ggcccttgag gaccagcca cacctcctgc 1560
ctctgaagga gaaagcccca gcagacccc gccagaggcg gcccggggcg caggccccac 1620
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<210> 92
<211> 505
<212> PRT
<213> H.Sapiens

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<400> 92

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20          25          30
Gly Pro Gln Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly
35          40          45
His Arg Pro Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly
50          55          60
Gly Trp Asp Thr Val Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro
65          70          75          80
Ala Asn Gly Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly
85          90          95
Ala Gly Thr Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp
100         105         110
Phe Leu Phe Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His
115         120         125
Gly Gly His Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe
130         135         140
Leu Trp Gly Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu
145         150         155         160

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## 00431PHRM293.ST25

Ser Leu Asp Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly  
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 His Arg Pro Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val  
 180 185 190  
 Leu Ala Thr Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala  
 195 200 205  
 Val Trp Trp Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu  
 210 215 220  
 Glu Leu Ser Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe  
 225 230 235 240  
 Leu Leu Leu Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg  
 245 250 255  
 Thr Cys His Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg  
 260 265 270  
 Val Ala Arg Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr  
 275 280 285  
 Gln Leu Ala Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser  
 290 295 300  
 Gly Tyr Leu Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu  
 305 310 315 320  
 Leu Asn Ser Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp  
 325 330 335  
 Leu Arg Thr Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu  
 340 345 350  
 Cys Glu Glu Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln  
 355 360 365  
 Leu Asp Ser Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln  
 370 375 380  
 Ser Gln Met Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln  
 385 390 395 400  
 Pro Arg Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln  
 405 410 415  
 Pro Gln Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln  
 420 425 430  
 Pro Gln Ser Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln  
 435 440 445  
 Thr Pro Ala Pro Ala Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala  
 450 455 460  
 Ser Pro Thr Pro Ser Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro  
 465 470 475 480



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1413

<210> 94  
 <211> 419  
 <212> PRT  
 <213> H.Sapiens

<400> 94

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 35 40 45  
 Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr  
 50 55 60  
 Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe  
 65 70 75 80  
 Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His  
 85 90 95  
 Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly  
 100 105 110  
 Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp  
 115 120 125  
 Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro  
 130 135 140  
 Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr  
 145 150 155 160  
 Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp  
 165 170 175  
 Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser  
 180 185 190  
 Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu  
 195 200 205  
 Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg Thr Cys His  
 210 215 220  
 Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg  
 225 230 235 240  
 Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala  
 245 250 255  
 Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu

260

265

270

Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser  
 275 280 285  
 Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr  
 290 295 300  
 Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu  
 305 310 315 320  
 Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser  
 325 330 335  
 Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met  
 340 345 350  
 Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser  
 355 360 365  
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser  
 370 375 380  
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser  
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<210> 97  
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<400> 97  
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<210> 98  
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<210> 99  
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<210> 100  
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<400> 100  
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<400> 110  
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<400> 113

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19

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19

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<400> 117  
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<210> 118  
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<400> 119  
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18

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<400> 133  
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<210> 134  
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 <212> DNA  
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<400> 134  
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23

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 ctatccaacg cactggtgct gctttgttgc gcctacagcg ctgagctccg cactcgagcc 180  
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 cccttcacgc tgctcggtgt gatgcgcggg cggacaccgt cggcgcccgg cgcattgcca 300  
 gtcattggct tcttggaac cttcctggcg tccaacgcgg cgctgagcgt ggcgggcgctg 360  
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 ccgcgcccag cgtccaccca caacggctct gtggacacag agaatgattc ctgcctgcag 1140  
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<400> 186

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 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu  
 35 40 45  
 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu  
 50 55 60  
 Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln  
 65 70 75 80  
 Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser  
 85 90 95  
 Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu  
 100 105 110  
 Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly  
 115 120 125  
 Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys  
 130 135 140  
 Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu  
 145 150 155 160  
 Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu  
 165 170 175  
 His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser  
 180 185 190  
 Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr  
 195 200 205  
 Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val

210

215

220

Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr  
 225 230 235 240

Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro  
 245 250 255

Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn  
 260 265 270

Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val  
 275 280 285

Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val  
 290 295 300

Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala  
 305 310 315 320

Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu  
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Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asn Gly Ser Val Asp  
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<400> 190  
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18